

Query= SEQ ID NO:3
(1047 letters)

Sequences producing significant alignments:

AC008121.33.67777.200926 546 e-153

>AC008121.33.67777.200926
Length = 133150

Score = 546 bits (275), Expect = e-153
Identities = 275/275 (100%)
Strand = Plus / Plus

Query: 382 agcgatccttaatgtggacagctgtgatttgaactaataatatacatggacgctatcct 441
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 51038 agcgatccttaatgtggacagctgtgatttgaactaataatatacatggacgctatcct 51097

Query: 442 cataccaagaagataaaaattaaagcaatcattattcatccaaacttcattttggaatct 501
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 51098 cataccaagaagataaaaattaaagcaatcattattcatccaaacttcattttggaatct 51157

Query: 502 tatgtaaatgatattgcacttttcactaaaaaaaggcagtgaggtataatgactatatt 561
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 51158 tatgtaaatgatattgcacttttcactaaaaaaaggcagtgaggtataatgactatatt 51217

Query: 562 cagcctatttgcctaccccttgcattttcaatcctggacggaaacacaaaagtgttt 621
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 51218 cagcctatttgcctaccccttgcattttcaatcctggacggaaacacaaaagtgttt 51277

Query: 622 ataagtggctgggaagaacaaaagaagaaggtaa 656
||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Sbjct: 51278 ataagtggctgggaagaacaaaagaagaaggtaa 51312

Score = 502 bits (253), Expect = e-139
Identities = 253/253 (100%)
Strand = Plus / Plus

Query: 795 gggtgacagtggggaccattaatgtgctacttaccagaatataaaagattttgtaat 854

Query: 796 gggatattaccaggtacgacatggctgtggcgaagaggtttctgggtctatattgg 7961
||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

Query: 915 gccatccttctacaaaagtggctacagagcattttccatgcaagcactcaaggcat 974
Sbjct: 79708 gccatccttctacaaaagtggctacagagcattttccatgcaagcactcaaggcat 79767

Query: 975 acttactataaatttacgtggccagatcctcatagcttatgtttgtcatctact 1034
Sbjct: 79768 acttactataaatttacgtggccagatcctcatagcttatgtttgtcatctact 79827

Query: 1035 agcaacaacataa 1047
Sbjct: 79828 agcaacaacataa 79840

Score = 387 bits (195), Expect = e-105
Identities = 196/197 (99%)
Strand = Plus / Plus

Query: 187 gattgtggaacagcaccgcttaaggatgtttgcaagggtctcgattataggggcacc 246
Sbjct: 36091 gattgtggaacagcaccgcttaaggatgtttgcaagggtctcgattataggggcacc 36150

Query: 247 gaagcacaagctggcgcatggccgtgggtggtgagcctgcagattaaatatggccgttt 306
Sbjct: 36151 gaagcacaagctggcgcatggccgtgggtggtgagcctgcagattaaatatggccgttt 36210

Query: 307 cttgttcatgtatgtggggaaaccctagtgagagagaggtgggtcctcacagctgcccac 366
Sbjct: 36211 cttgttcatgtatgtggggaaaccctagtgagagagaggtgggtcctcacagctgcccac 36270

Query: 367 tgcactaaagacrctag 383
Sbjct: 36271 tgcactaaagacactag 36287

Score = 363 bits (183), Expect = 9e-98
Identities = 185/187 (98%)
Strand = Plus / Plus

Query: 1 atgcggctgggctcctgagcgtggcggtttgtggggagctctacttayactca 60

Sbjct: 36275 gaccaactactcgccctctggaaaggcacaggctcgcccccctggggaaacggggtagt 36334

Query: 121 tcccagcaggctgaggccgtccgcaagaggctccggcggcggagggagggagggcgcat 180
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 35335 tcccagcaggctgaggccgtccgcaagaggctccggcggcggagggagggagggcgcat 35394

Query: 181 gcaaagg 187
|||||||
Sbjct: 35395 gcaaagg 35401

Score = 290 bits (146), Expect = 1e-75
Identities = 146/146 (100%)
Strand = Plus / Plus

Query: 651 aggtaacgcataaaatatttacaagatgcagaagtgcattatattctcgagagatgtg 710
||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 77571 aggtaacgcataaaatatttacaagatgcagaagtgcattatattctcgagagatgtg 77630

Query: 711 taattctgagaggagttatggggaataattcctaacaacttcatttgcaggtatga 770
||||||||||||||||||||||||||||||||||||||||||||||||||||
Sbjct: 77631 taattctgagaggagttatggggaataattcctaacaacttcatttgcaggtatga 77690

Query: 771 agatggagctttgataacttgcaagg 796
||||||||||||||||||||||||
Sbjct: 77691 agatggagctttgataacttgcaagg 77716

>XM_171629 ACCESSION:XM_171629 NID: gi 22062231 ref XM_171629.1 Homo sapiens similar to cortical granule serine protease 1 precursor (LOC257238), mRNA
Length = 1295

Identities = 141/153 (92%), Positives = 141/153 (92%)
Frame = +3

Query: 62 CGTAPLKDVLQGSRIIGGTEAQAGAWPWVSLQIKYGRVLVHVCGGTLVRERWLTAHC 121
CGTAPLKDVLQGSRIIGGTEAQAGAWPWVSLQIKYGRVLVHVCGGTLVRE
Sbjct: 3 CGTAPLKDVLQGSRIIGGTEAQAGAWPWVSLQIKYGRVLVHVCGGTLVRE----- 155

Query: 122 TKDSDPLMWTAIGTNNIHGRYPHTKKIKIKAIHHPNFILESYVNDIALFHLKKAVRYN 181
SDPLMWTAIGTNNIHGRYPHTKKIKIKAIHHPNFILESYVNDIALFHLKKAVRYN
Sbjct: 156 ---SDPLMWTAIGTNNIHGRYPHTKKIKIKAIHHPNFILESYVNDIALFHLKKAVRYN 326

Query: 182 DYIQPICLPDFVQILDGNTKCFISGWGRTEE 214
DYIQPICLPDFVQILDGNTKCFISGWGRTEE
Sbjct: 327 DYIQPICLPDFVQILDGNTKCFISGWGRTEE 427

Identities = 131/131 (100%), Positives = 131/131 (100%)
Frame = +3

Query: 215 GNATNILQDAEVHYISREMCNSERSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLP 274
GNATNILQDAEVHYISREMCNSERSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLP
Sbjct: 900 GNATNILQDAEVHYISREMCNSERSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLP 1079

Query: 275 EYKRFFVMGITSYGHGCRRGFPGVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILI 334
EYKRFFVMGITSYGHGCRRGFPGVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILI
Sbjct: 1080 EYKRFFVMGITSYGHGCRRGFPGVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILI 1259

Query: 335 ALCFVILLATT 345
ALCFVILLATT
Sbjct: 1260 ALCFVILLATT 1292



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1: XM_171629. Homo sapiens simi...[gi:22062231]

Links

LOCUS LOC257238 1295 bp mRNA linear PRI 01-AUG-2002
DEFINITION Homo sapiens similar to cortical granule serine protease 1 precursor (LOC257238), mRNA.
ACCESSION XM_171629
VERSION XM_171629.1 GI:22062231
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1295)
AUTHORS NCBI Annotation Project.
TITLE Direct Submission
JOURNAL Submitted (31-JUL-2002) National Center for Biotechnology Information, NIH, Bethesda, MD 20894, USA
COMMENT GENOME ANNOTATION REFSEQ: This model reference sequence was predicted from NCBI contig NT_009782 by automated computational analysis using gene prediction method: GenomeScan, supported by EST evidence.
Also see:
[Documentation of NCBI's Annotation Process](#)

FEATURES Location/Qualifiers
source 1..1295
/organism="Homo sapiens"
/db_xref="taxon:9606"
/chromosome="12"
gene 1..1295
/gene="LOC257238"
/db_xref="InterimID:257238"
CDS 168..1295
/gene="LOC257238"
/codon_start=1
/product="similar to cortical granule serine protease 1 precursor"
/protein_id="XP_171629.1"
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/note="Region: smart00020, Tryp_SPC, Trypsin-like serine protease; Many of these are synthesised as inactive precursor zymogens that are cleaved during limited proteolysis to generate their active forms. A few, however, are active as single chain molecules, and others are inactive due to substitutions of the catalytic triad residues"

misc_feature
171..434
/gene="LOC257238"
/note="Region: pfam00089, trypsin, Trypsin"

misc_feature
819..1199
/gene="LOC257238"
/note="Region: pfam02395, IGA1, Immunoglobulin A1 protease. This family consists of immunoglobulin A1 protease proteins. The immunoglobulin A1 protease cleaves immunoglobulin IgA and is found in pathogenic bacteria such as *Neisseria gonorrhoeae*. Not all of the members of this family are IgA proteases (one member from *E. coli* cleaves human coagulation factor V, another one is a hemoglobin protease)"

misc_feature
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/gene="LOC257238"
/note="Region: smart00020, Tryp_SPC, Trypsin-like serine protease; Many of these are synthesised as inactive precursor zymogens that are cleaved during limited proteolysis to generate their active forms. A few, however, are active as single chain molecules, and others are inactive due to substitutions of the catalytic triad residues"

misc_feature
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variation
681
/gene="LOC257238"
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/allele="T"
/db_xref="dbSNP:3742071"

BASE COUNT 352 a 265 c 314 g 364 t
ORIGIN

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61 aagcacaAGC tggcgcatGG ccgtgggtGG tgagcctGCA gattaaatAT ggcgcgtGTC  
121 ttgttcatGT atgtggggGA accctagtGA gagagAGcGA tcctttaATG tggacagCTG  
181 tgattggAAC taataatATA catggacGCT atcctcatac caagaagata aaaattaaAG  
241 caatcattAT tcatccaaAC ttcatTTG aatcttatGT aaatgatATT gcactTTTC  
301 acttaaaaaAA agcagtGAGG tataatGACT atattcAGCC tatttgCCTA ccttttgatG  
361 ttttccaaAT cctggacGGA aacacaaAGT gttttataAG tggctgggGA agaacaaaAG  
421 aagaaggTAT agcaggGCTT gtgactgtGG tgcctgtGG tctttacaAG ctaaagtaca  
481 gaagagatCA gaaaatgtCA attcatCTTA ttcacatGAG agttgcgtGCC caaggattTG  
541 ttgttggAGC tgtgactCTA gctcgaggCT ttgcaggAGG cgcacacTGC atggccttAC  
601 cggcaggTGA gcccggcGGG ctctcatCGC ctcagccGGA gattccaACT gcagggagcG
```

1261 ctttatgttt tgtcatctta ctagcaacaa cataaa
//

Revised: July 5, 2002.

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Dec 2 2002 13:45:47

>XM_208689 ACCESSION:XM_208689 NID: gi 30157117 ref XM_208689.3
Homo sapiens similar to adrenal secretory serine
protease precursor (LOC283471), mRNA
Length = 1457

Score = 712 bits (1819), Expect = 0.0
Identities = 344/348 (98%), Positives = 345/348 (98%), Gaps = 3/348 (0%)
Frame = +1

Query: 1 MRLGLLSVAL-FVGSSHL-SDHYSPSGRHLGSPPEPAASSQQAEAVRKRLRRRREGGAH 58
MRLGLLSVAL FVGSSHL SDHYSPSGRHLGSPPEPAASSQQAEAVRKRLRRRREGGAH
Sbjct: 40 MRLGLLSVALFVGSSHLYSDHYSPSGRHLGSPPEPAASSQQAEAVRKRLRRRREGGAH 219

Query: 59 AKDCGTAPLKDVLQGSRIIGGTEAQAGAWPVVSLQIKYGRVLVHVCGGTLVRERWVLT A 118
A+DCGTAPLKDVLQGSRIIGGTEAQAGAWPVVSLQIKYGRVLVHVCGGTLVRERWVLT
Sbjct: 220 AEDCGTAPLKDVLQGSRIIGGTEAQAGAWPVVSLQIKYGRVLVHVCGGTLVRERWVLT A 399

Query: 119 AHCTKD-SDPLMWTAIGTNNIHGRYPHTKKIKIKAIIIHPNFILESYVNDIALFHLKKA 177
AHCTKD SDPLMWTAIGTNNIHGRYPHTKKIKIKAIIIHPNFILESYVNDIALFHLKKA
Sbjct: 400 AHCTKDASDPLMWTAIGTNNIHGRYPHTKKIKIKAIIIHPNFILESYVNDIALFHLKKA 579

Query: 178 VRYNDYIQPICLPDFVQILDGNTKCFISGWGRTEEGNATNILQDAEVHYISREMCNSE 237
VRYNDYIQPICLPDFVQILDGNTKCFISGWGRTEEGNATNILQDAEVHYISREMCNSE
Sbjct: 580 VRYNDYIQPICLPDFVQILDGNTKCFISGWGRTEEGNATNILQDAEVHYISREMCNSE 759

Query: 238 RSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLPEYKRFVVMGITSYGHGCGRRGFP 297
RSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLPEYKRFVVMGITSYGHGCGRRGFP
Sbjct: 760 RSYGGIIPNTSFCAGDEDGAFDTCRGDSGGPLMCYLPEYKRFVVMGITSYGHGCGRRGFP 939

Query: 298 GVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILIALCFVILLATT 345
GVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILIALCFVILLATT
Sbjct: 940 GVYIGPSFYQKWLTEHFFHASTQGILTINILRGQILIALCFVILLATT 1083


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    /gene="LOC283471"
    /note="COG5640; Region: Secreted trypsin-like serine
protease [Posttranslational modification, protein
turnover, chaperones]"
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misc_feature
268..978
/gene="LOC283471"
/note="Tryp_SPC; Region: Trypsin-like serine protease"
/db_xref="CDD:smart00020"
misc_feature
271..978
/gene="LOC283471"
/note="trypsin; Region: Trypsin"
/db_xref="CDD:pfam00089"
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BASE COUNT 419 a 269 c 327 g 442 t

ORIGIN

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61 gtggcgtgt tgtttggg gagctctcac ttatactcag accactactc gcctctggc
121 aggacacaggc tcggccctc gcccgaacgg gcggctagtt cccagcaggc tgaggccgtc
181 cgcaagagggc tccggcggcg gaggggaggga gggggcgtatc cagaggattt tgaaacagca
241 cccgcttaagg atgtgttgca agggctctgg attatagggg gcaccgaagc acaagctggc
301 gcatggccgt gggtggtgag cctgcagatt aaatatggcc gtgttcttgt tcatgtatgt
361 gggggaaacc tagtgagaga gaggtgggtc ctcacagctg cccactgcac taaagacgct
421 agcgatcctt taatgtggac agctgtgatt ggaactaata atatacatgg acgtatcct
481 cataccaaga agataaaaat taaagcaatc attattcatc caaacttcat tttgaaatct
541 tatgtaaatg atattgcact tttcacttta aaaaaagcag tgaggtataa tgactatatt
601 cagccttattt gcctacccccc ttgtatgggcaaaatcctgg acggaaacac aaagtgtttt
661 ataagtggct ggggaagaac aaaagaagaa ggtaacgcta caaatatttt acaagatgca
721 gaagtgcatt atattctcg agagatgtgt aattctgaga ggagttatgg gggaaataatt
781 cctaacactt cattttgtgc aggtgtatgaa gatggagctt ttgatacttg caggggtgac
841 agtgggggac cattaatgtc ctacttacca gaataaaaaa gattttttgt aatgggaaatt
901 accagttacg gacatggctg tggcgaaga ggtttccctg gtgtctatata tggccatcc
961 ttctaccaaa agtggctgac agagcatttc ttccatgcaa gcactcaagg catacttact
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1081 acataaaagaa attctgaagg ctttcatatc tttatttgc attgtgtccc ttctatgtt
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1201 tgaacatttt atgggtata agtattgtga cagatataca attgtatattt tggcactgaa
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1381 aatagtttat aattaaaatg aagctgtca tttggtaaa ttaataaaaaa ttctttctta
1441 gatttttattt taaaaaaa

11

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May 2 2003 16:47:12